

10 B.2

# Gap Results

**Refine**GAP of: 1169\_seq\_10 check: 1278 from: 1 to: 3792to: 1169\_seq\_2 check: 3043 from: 1 to: 1638Symbol comparison table: nwsgapdna.cmp CompCheck: 8760

Gap Weight:	50	Average Match:	10.000
Length Weight:	3	Average Mismatch:	0.000

Quality:	5384	Length:	3793
Ratio:	3.287	Gaps:	17
Percent Similarity:	40.134	Percent Identity:	40.134

Match display thresholds for the alignment(s):

	=	IDENTITY
:	=	5
.	=	1

1169\_seq\_10 x 1169\_seq\_2 March 19, 2003 16:09 ..

```
901 tttcgcattgtatcagaatggcgaggttgccgacgttgcaaagtctttac 950
      ||| | | | | | | | | |
1 .....atgtcgccaccagcaactccagaggcgattgttccgtcgcatg 44
      . . . . .
951 tgttgcctttccgtcaccttagcagccacgtccatctcaatgcttgccg 1000
      | | | | | | | | | |
45 cgacgccatcatcggttgagccggcctcagcggcatctctgctgtgtaca 94
      . . . . .
1001 cttcaggttcagtcgtttaccaacgccgcacgttccggtccgaattattc 1050
      | | | | | | | | | |
95 aattgcgaaagctcagactcaacgccaaaatcttcgagggagccccgat 144
      . . . . .
1051 agtatcattgacaaaaccacgcagctcgaccctctcgacccttctggaaa 1100
      | | | | | | | | | |
145 tttggcggcgtctggcactggaaccgctaccctggcgtcgtgttgattc 194
      . . . . .
1101 gcagccagagggctgcctaggtcaaattgagatccaaaacctggcatttg 1150
      | | | | | | | | | |
195 ggagacgcccttctaccaactgaacattcccgaagtatggaaagactgga 244
      . . . . .
1151 cctacccctcccgaccatctgcccagttacttcgagatttcaacttgaca 1200
      ||| | | ||| ||| ||| |||
245 cctgggtcttgccgctatcctgacca.....gaaagagttg 279
      . . . . .
1201 attccagctggcaagacgacggccctcgctcggtgcatcaggtagcggcaa 1250
      | | | | | | | | | |
280 ctgtcatatgttcaccactgtgacaagatccggggcttgagaaaagacgt 329
      . . . . .
1251 aagcacaatggtcggttacttgaacggtggtatctgccagttcggggga 1300
      | | | | | | | | | |
```

```
330 ctacttcggagctgaggtggttgatgcgcggtat.gccagagatctgggc 378
      . . . . .
1301 ggatattacttgatgggttggaactgggacaataacaatgtgaaatggctg 1350
      | | | | | | | | | |
379 acctggactgtcaagacgtcggctggccatgttgcgacggcaaagtatct 428
      . . . . .
1351 agaagccgcattcgcctcggttaacaggaacctgtgtgtttcgtggcac 1400
      ||| | | | | | | | | |
429 cattctcgctacggggttgctccacaggaagcacact.....cc 467
      . . . . .
1401 aatcttccagaacattgccaacggtttcatggatgagcaacgagatctgc 1450
      ||| | | | | | | | | |
468 cgcactccccggcctcgccgatttcaacgggaaggtgattcattcgagtg 517
      . . . . .
1451 ctcgcgaaaaacaaatggagcttggtgcaaaaagcttgcaaagccagcaat 1500
      | | | | | | | | | | | |
518 cctggcacgaagacttcgacgcagagggccagagagtcgccgtcatcggt 567
      . . . . .
1501 ggcgacgtgttcattaatgagcttccgaacggttatgagactgaagttgg 1550
      | | | | | | | | | | | |
568 gccggggccacaagcatccagattgttcaggagttggccaagaaggctga 617
      . . . . .
1551 cgagcgagccggagccttgagtggaggtcaacgacaacgaattgcaatcg 1600
      | | | | | | | | | | | |
618 ccaggtaacc.....atgtttatgcaaggccgagctattgtctgcc 659
      . . . . .
1601 cacgaagtatcatatcggatcccaagatcctgttactcgatgaagctacc 1650
      ||| | | | | | | | | |
660 catgcggcaacgaa.....cgatggataggaacgaacagacagcctgg 702
      . . . . .
```

```
1651 agcgcccttgacccgaaggcggagaaagtgggccaggaggccttgaaccg 1700
      | ||| |||| | | | ||| | | ||| || |
703 aaggcctactacccacgctgtttgaagcgagtcgaaagtctcggattgg 752
      . . . . .
1701 agtgtccaaagaccgcactactttggtcattgccacaaaactagccactg 1750
      | | | ||| | | ||| | ||| ||| |
753 a...ttcccggtccaggcaccgctcggttggcatctttgaagtcagccccg 799
      . . . . .
1751 tcaaaagtgtggcaacatcgcagtcatttcccaggggaaaatcgtcgag 1800
      | | | | | ||| | | ||| | | |
800 agcagcgggaggcctatttcgaagagttgtgggagcgtggggcctttaat 849
      . . . . .
1801 caaggcacacaccacgaattgatcgaattcggtgtcattacgccgcact 1850
      | ||| | | || |||| | | | ||
850 tttcttgcttgcca.gtaccgagaagtcaggttgacaaaaaggccaacc 898
      . . . . .
1851 ggtgcgtgcacaggacctcggggctgacgaacaacaagaacatgagaaga 1900
      | || | ||| | || || || |
899 gactggtctatgacttctgggccaaaaagactcgatctcgtatcgtcaat 948
      . . . . .
1901 ccctgcacgaaaaggcagcacgagaagctgctggtgaacgaccggcactt 1950
      || | ||| | | ||| | | |||| |
949 ccggcaaagagagatctcatggctcctctggagccgccgtactgggttcgg 998
      . . . . .
1951 gagcgactcacaccactgccacatctcaagctggaga.cctggagaagc 1999
      | | | | | |||| | | ||| |||| |
999 taccaagcgctccccactggagagcgactactacgaaatgctggacaagc 1048
      . . . . .
2000 ggaaggtgccggtcgggactttgggctactcgctcctaaaatgcaccta 2049
      || || | | | | | |||| |
```

```
1049 cgagcgtcgaaattgtgaatctagaacaatcgccc..... 1083
      .      .      .      .      .
2050 atcatgttctacgaacaaaaaatctctactgggtgcttcttgtgtcaac 2099
      || |      | ||| |      || | |      || | || |
1084 .....attgtggctgttaciaaagacaggtgtgctcttgagtgcgcgcagc 1128
      .      .      .      .      .
2100 aataacggttctgatatgcgcggccacatttccaggacaagcccttttgt 2149
      || | | | || | | || |      | |      ||
1129 aagagggaatgcgacacgatcgtgc.....tggcgacgggt 1164
      .      .      .      .      .
2150 tttcgagattgctcactgtcttcgagttgagtggcatgcggcacaggaa 2199
      ||      || | |      || | ||      || | ||      || | |
1165 ttcgacagtttctactggctcattgacacatatgggcttgaaaaacaagca 1214
      .      .      .      .      .
2200 cgggcagacttttatattctgatgttctttgtcgtggctctaggaaatct 2249
      |||      | | | | | | | |      | |      || | |
1215 cgg.....agtggacctgaaggaggtgtggaaagatggcatatctactta 1259
      .      .      .      .      .
2250 agtaggatatttcacgattggctggacatgcaacgttatttcacaagttg 2299
      | |||      ||| |      |||      | | | | |      || |
1260 tatgggagtccttctctcatggc.....ttccccaatgccttcttcgtcg 1303
      .      .      .      .      .
2300 tcacccatcgctatcaagccgcaatgttccaacgagtactggatcaagac 2349
      |||      ||      |      |||      | | | | |      | |      |||
1304 ccacgggtcaagccccgaccgtcctttccaacggcccaacgatcatagaa 1353
      .      .      .      .      .
2350 atcgaactcctcgacatcccggagcaaatttctgggtgctctcacatcgca 2399
      | | || || |      ||| | ||      |||      | | |
1354 acccaagtcgacttgatcgccgatacaatt.....gcaaagtt 1391
      .      .      .      .      .
```

2400 actgtcagctctacccacgcagttgcaagagttgatatcagcaaattttc 2449

| | | | | | | | | | | | | | | |

1392 ggaggccgagcagccacgtccgttgaggcgacgaaatcagcaca.agag 1440

. . . . .

2450 tcatttatatcgttgtcggcgaacatcgctcgcagcagtgctctaccact 2499

| | | | | | | | | | | | | | | |

1441 gcatggtcgattatgattgccaagatgaacgagcacactctgttcccctt 1490

. . . . .

2500 agcctatggatggaaactgggcctggtggttggttggtgcacttccac 2549

| | | | | | | | | | | | | | | |

1491 gacggattcgtgg.....tggactggaggcaacatccctgggaaagcaac 1535

. . . . .

2550 ccctgcttttggctggctacctcagaattcgtctagagacgaagctagaa 2599

| | | | | | | | | | | | | | | |

1536 acgtgctttaaccttcata.ggcgggattgctctctatgagcagatctgt 1584

. . . . .

2600 gccggaaactcggcaaactttgcagaaagtgcctgggcttgcaagcgaagc 2649

| | | | | | | | | | | | | | | |

1585 caagagaaggtggccaattgggatgggtttgatgtgctt.catgctccct 1633

. . . . .

2650 agttaccgcatccggaccgtctcatctttgactctcgaaggccatgttc 2699

| |

1634 gctaa..... 1638

.

.

.

**Input Sequence: 1169\_seq\_10**

```
!!NA_SEQUENCE 1.0

1169_seq_10 Length: 3792 March 19, 2003 16:05 Type: N
Check: 1278 ..

      1 atggcagatg aatcggagaa acctcgacca aaccaagatg
gcagtgagtc
```

[View Sequence](#)

## Input Sequence: 1169\_seq\_2

```
!!NA_SEQUENCE 1.0

1169_seq_2 Length: 1638 March 19, 2003 16:04 Type: N
Check: 3043 ..

      1 atgtcggcca ccagcaactc cagaggcgat tgttcgctcg
catgcgacgc
```

[View Sequence](#)





# Gap Results

**Refine**

GAP of: seq 3 check: 4503 from: 1 to: 545

to: seq 8 check: 1671 from: 1 to: 525

Symbol comparison table: blosum62.cmp CompCheck: 1102

BLOSUM62 amino acid substitution matrix.

Reference: Henikoff, S. and Henikoff, J. G. (1992). Amino acid  
substitution matrices from protein blocks. Proc. Natl. Acad.  
Sci. USA 89: 10915-10919.

Gap Weight:	8	Average Match:	2.778
Length Weight:	2	Average Mismatch:	-2.248

Quality:	7	Length:	1044
Ratio:	0.013	Gaps:	2
Percent Similarity:	30.769	Percent Identity:	26.923

Match display thresholds for the alignment(s):

| = IDENTITY

: = 2

. = 1

seq 3 x seq 8

March 20, 2003 10:46 ..

1 .....MS 2

451 VNVLAVVFTSVTTVFFSFPLTVPTAASTMNYTSAIIGVALALGVLNWVVH 500

3 ATSNSRGDCSVACDAIIVGAGLS.GISAVYKLRKLRLNAKIFEGAPDFGG 51

| . .| . | :||| |

501 ARKHYQGP.HLELDGRVVGAEFQVGP..... 525

### Input Sequence: seq\_3

```
!!AA_SEQUENCE 1.0
seq_3 Length: 545 March 20, 2003 10:41 Type: P Check:
4503 ..

1 MSATSNSRGD CSVACDAIIV GAGLSGISAV YKLRKLRLNA
KIFEGAPDFG
```

[View Sequence](#)

## Input Sequence: seq\_8

```
!!AA_SEQUENCE 1.0
    seq_8 Length: 525 March 20, 2003 10:42 Type: P Check:
1671 ..

      1 MDSRPSGYGE KGGTRQTTKN TETAAAGGAS ESLNVPLEKK
QFGTITIVSL
```

[View Sequence](#)